to grow at 37 °C until an OD 600 of about 0.5 is reached. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P510S-C construct are shown in SEQ ID NO: 823 and 826, respectively.

The predicted third extracellular domain of P510S (P510S-E3; residues 328-676 of SEQ ID NO: 538) was expressed in *E. coli* as follows. The P510S fragment was amplified by PCR using the primers shown in SEQ ID NO: 830 and 831. The primer of SEQ ID NO: 830 is a sense primer with an NdeI site for use in ligating into pPDM. The primer of SEQ ID NO: 831 is an antisense primer with an added XhoI site for use in ligating into pPDM. The resulting fragment was cloned to pPDM at the NdeI and XhoI sites. Clones were confirmed by sequencing. For protein expression, the clone ws transformed into E. coli BL21 (DE3) CodonPlus-RIL competent cells. After induction, an OD600 of greater than 2.0 was achieved after 3 hours. Coomassie stained SDS-PAGE showed an over-expressed band at about 39 kD, and N-terminal sequencing confirmed the N-terminal to be that of P510S-E3. Optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2x YT. Allow to grow at 37 °C until OD 600 equals 0.6. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3 sample, spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P501S-E3 construct are provided in SEQ ID NO: 824 and 827, respectively.

g) Expression of P775S in *E. Coli*

The antigen P775P contains multiple open reading frames (ORF). The third ORF, encoding the protein of SEQ ID NO: 483, has the best emotif score. An expression fusion construct containing the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 819) and P775P-ORF3 with an N-terminal 6x HisTag was prepared as follows. P775P-ORF3 was amplified using the sense PCR primers of SEQ ID NO: 832 and the anti-sense PCR primer of SEQ ID NO: 833. The PCR amplified fragment of P775P and

Ra12/pCRX1 were digested with the restriction enzymes EcoRI and XhoI. Vector and insert were ligated and then transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. A clone having the desired sequence was transformed into E. coli BL21 (DE3) CodonPlus-RIL competent cells. Two hours after induction, the cell density peaked at OD600 of approximately 1.8. Coomassie stained SDS-PAGE showed an over-expressed band at about 31 kD. Western blot using 6x HisTag antibody confirmed that the band was Ra12-P775P-ORF3. The determined cDNA and amino acid sequences for the fusion construct are provided in SEQ ID NO: 834 and 835, respectively.

H) Expression of a P703P His tag fusion protein in *E. coli*

The cDNA for the coding region of P703P was prepared by PCR using the primers of SEQ ID NO: 836 and 837. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P703P are provided in SEQ ID NO: 838 and 839, respectively.

I) Expression of a P705P His tag fusion protein in *E. coli*

The cDNA for the coding region of P705P was prepared by PCR using the primers of SEQ ID NO: 840 and 841. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P705P are provided in SEQ ID NO: 842 and 843, respectively.

J) Expression of a P711P His tag fusion protein in *E. coli*

The cDNA for the coding region of P711P was prepared by PCR using the primers of SEQ ID NO: 844 and 845. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P711P are provided in SEQ ID NO: 846 and 847, respectively.

K) Expression of P767P in *E. coli*

The full-length coding region of P767P (amino acids 2-374 of SEQ ID NO: 590) was amplified by PCR using the primers PDM-468 and PDM-469 (SEQ ID NO: 935 and 936, respectively). DNA amplification was performed using 10 µl 10X Pfu buffer, 1 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM concentration, 83 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 20 sec, 66°C for 15 sec and by 72°C for 2 min., and lastly by 1 cycle of 72°C for 4 min. The PCR product was digested with XhoI and cloned into a modified pET28 vector with a histidine tag in frame on the 5' end that was digested with Eco72I and XhoI. The construct was confirmed to be correct through sequence analysis and transformed into *E. coli* BL21 pLysS and BL21 CodonPlus RP cells. The cDNA coding region for the recombinant B767P protein is provided in SEQ ID NO: 938, with the corresponding amino acid sequence being provided in SEQ ID NO: 941. The full-length P767P did not express at high enough levels for detection or purification.

A truncated coding region of P767P (referred to as B767P-B; amino acids 47-374 of SEQ ID NO: 590) was amplified by PCR using the primers PDM-573 and PDM-469 (SEQ ID NO: 937 and 936, respectively) and the PCR conditions described above for full-length P767P. The PCR product was digested with XhoI and cloned into the modified pET28 vector that was digested with Eco72I and XhoI. The

construct was confirmed to be correct through sequence analysis and transformed into *E. coli* BL21 pLysS and BL21 CodonPlus RP cells. The protein was found to be expressed in the inclusion body pellet. The coding region for the expressed B767P-B protein is provided in SEQ ID NO: 939, with the corresponding amino acid sequence being provided in SEQ ID NO: 940.

EXAMPLE 18

PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

a) Preparation and Characterization of Polyclonal Antibodies against P703P, P504S and P509S

Polyclonal antibodies against P703P, P504S and P509S were prepared as follows.

Each prostate tumor antigen expressed in an *E. coli* recombinant expression system was grown overnight in LB broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml to 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nm) of the culture reached 0.4-0.6, the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty ml of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed

inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

As a final purification step, a strong anion exchange resin such as HiPrepQ (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off the column with a increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The proteins were then vialed after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

Four hundred micrograms of each prostate antigen was combined with 100 micrograms of muramyldipeptide (MDP). Every four weeks rabbits were boosted with 100 micrograms mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animal was bled. Sera was generated by incubating the blood at 4°C for 12-4 hours followed by centrifugation.

Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) of recombinant protein at 4 °C for 20 hours. 250 microliters of BSA blocking buffer was added to the wells and incubated at room temperature for 2 hours. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at room temperature for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at room temperature for 30 min. Plates were again

washed as described above and 100 microliters of TMB microwell peroxidase substrate was added to each well. Following a 15 min incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H_2SO_4 and read immediately at 450 nm. All polyclonal antibodies showed immunoreactivity to the appropriate antigen.

b) Preparation and Characterization of Antibodies against P501S

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO: 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody component were sacrificed and spleen cells were used to generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant (μg/ml)
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis. Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1 μg/ml, followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8 as a control antigen and either fixed and permeabilized as described

above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity that DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr. HRP-labeled anti-

mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L)Affinipure F(ab') fragment (Jackson Immunoresearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors,

5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

c) Preparation and Characterization of Antibodies against P503S

A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows. The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further 15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using at ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to cell surface epitopes. Cells stably transfected with a control plasmid were employed as a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur

fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall bladder, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with each of the anti-P503S monoclonal antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

d) Preparation and Characterization of Antibodies against P703P

Rabbits were immunized with either a truncated (P703Ptr1; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptr1 attached to a solid support. Rabbit monoclonal antibodies were isolated using SLAM

technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk-/- cells either untransfected or transfected with a plasmid expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure

specificity, lysates from HEK293 cells stably transfected with a control plasmid were also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues tested (breast tumor, lung tumor and normal kidney).

e) Preparation and Characterization of Antibodies against P504S

Full-length P504S (SEQ ID NO: 108) was expressed and purified from bacteria essentially as described above for P501S and employed to raise rabbit monoclonal antibodies using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). The anti-P504S monoclonal antibody 13H4 was shown by Western blot to bind to both expressed recombinant P504S and to native P504S in tumor cells.

Immunohistochemical studies using 13H4 to assess P504S expression in various prostate tissues were performed as described above. A total of 104 cases, including 65 cases of radical prostatectomies with prostate cancer (PC), 26 cases of prostate biopsies and 13 cases of benign prostatic hyperplasia (BPH), were stained with the anti-P504S monoclonal antibody 13H4. P504S showed strongly cytoplasmic granular staining in 64/65 (98.5%) of PCs in prostatectomies and 26/26 (100%) of PCs in prostatic biopsies. P504S was stained strongly and diffusely in carcinomas (4+ in 91.2% of cases of PC; 3+ in 5.5%; 2+ in 2.2% and 1+ in 1.1%) and high grade prostatic intraepithelial neoplasia (4+ in all cases). The expression of P504S did not vary with Gleason score. Only 17/91 (18.7%) of cases of NP/BPH around PC and 2/13 (15.4%) of BPH cases were focally (1+, no 2+ to 4+ in all cases) and weakly positive for P504S in large glands. Expression of P504S was not found in small atrophic glands, postatrophic hyperplasia, basal cell hyperplasia and transitional cell metaplasia in either biopsies or prostatectomies. P504S was thus found to be over-expressed in all Gleason scores of prostate cancer (98.5 to 100% of sensitivity) and exhibited only focal positivities in

large normal glands in 19/104 of cases (82.3% of specificity). These findings indicate that P504S may be usefully employed for the diagnosis of prostate cancer.

EXAMPLE 19

CHARACTERIZATION OF CELL SURFACE EXPRESSION AND CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains. Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as described by Tusnady and Simon (Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol. 283*:489-506, 1998).

Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519, which is identical to the peptide of SEQ ID NO: 518 with the exception of the substitution of the histidine with an asparginine, was synthesized as described above. A

Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisol:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 μg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (*i.e.*, intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1 complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C.

Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g (internal membrane) fraction and also in the 100,000g (plasma membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 μg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng - 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of

SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above. To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

In further studies, mouse monoclonal antibodies were raised against amino acids 296 to 322 to P501S, which are predicted to be in an extracellular domain. A/J mice were immunized with P501S/adenovirus, followed by subsequent boosts with an *E. coli* recombinant protein, referred to as P501N, that contains amino acids 296 to 322 of P501S, and with peptide 296-322 (SEQ ID NO: 898) coupled with KLH. The mice were subsequently used for splenic B cell fusions to generate anti-peptide hybridomas. The resulting 3 clones, referred to as 4F4 (IgG1,kappa), 4G5 (IgG2a,kappa) and 9B9 (IgG1,kappa), were grown for antibody production. The 4G5 mAb was purified by passing the supernatant over a Protein A-sepharose column,

followed by antibody elution using 0.2M glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8, and buffer exchanged into PBS.

For ELISA analysis, 96 well plates were coated with P501S peptide 296-322 (referred to as P501-long), an irrelevant P775 peptide, P501S-N, P501TR2, P501S-long-KLH, P501S peptide 306-319 (referred to as P501-short)-KLH, or the irrelevant peptide 2073-KLH, all at a concentration of 2 ug/ml and allowed to incubate for 60 minutes at 37 °C. After coating, plates were washed 5X with PBS + 0.1% Tween and then blocked with PBS, 0.5% BSA, 0.4% Tween20 for 2 hours at room temperature. Following the addition of supernatants or purified mAb, the plates were incubated for 60 minutes at room temperature. Plates were washed as above and donkey anti-mouse IgHRP-linked secondary antibody was added and incubated for 30 minutes at room temperature, followed by a final washing as above. TMB peroxidase substrate was added and incubated 15 minutes at room temperature in the dark. The reaction was stopped by the addition of 1N H_2SO_4 and the OD was read at 450 nM. All three hybrid clones secreted mAb that recognized peptide 296-322 and the recombinant protein P501N.

For FACS analysis, HEK293 cells were transiently transfected with a P501S/VR1012 expression constructs using Fugene 6 reagent. After 2 days of culture, cells were harvested and washed, then incubated with purified 4O5 mAb for 30 minutes on ice. After several washes in PBS, 0.5% BSA, 0.01% azide, goat anti-mouse Ig-FITC was added to the cells and incubated for 30 minutes on ice. Cells were washed and resuspended in wash buffer including 1% propidium iodide and subjected to FACS analysis. The FACS analysis confirmed that amino acids 296-322 of P501S are in an extracellular domain and are cell surface expressed.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server

(http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al. Science 274*:1371-1374, 1996 and Berthon *et al. Am. J. Hum. Genet. 62*:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

EXAMPLE 20

REGULATION OF EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

Steroid (androgen) hormone modulation is a common treatment modality in prostate cancer. The expression of a number of prostate tissue-specific antigens have previously been demonstrated to respond to androgen. The responsiveness of the prostate-specific antigen P501S to androgen treatment was examined in a tissue culture system as follows.

Cells from the prostate tumor cell line LNCaP were plated at 1.5×10^6 cells/T75 flask (for RNA isolation) or 3×10^5 cells/well of a 6-well plate (for FACS analysis) and grown overnight in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum (BRL Life Technologies, Gaithersburg, MD). Cell culture was continued for an additional 72 hours in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum, with 1 nM of the synthetic androgen Methyltrienolone (R1881; New England Nuclear) added at various time points. Cells were then harvested for RNA isolation and FACS analysis at 0, 1, 2, 4, 8, 16, 24, 28 and 72-hours post androgen addition. FACS analysis was performed using the anti-P501S antibody 10E3-G4-D3 and permeabilized cells.

For Northern analysis, 5-10 micrograms of total RNA was run on a formaldehyde denaturing gel, transferred to Hybond-N nylon membrane (Amersham Pharmacia Biotech, Piscataway, NJ), cross-linked and stained with methylene blue. The filter was then prehybridized with Church's Buffer (250 mM Na_2HPO_4, 70 mM H_3PO_4, 1 mM EDTA, 1% SDS, 1% BSA in pH 7.2) at 65 °C for 1 hour. P501S DNA was

labeled with 32P using High Prime random-primed DNA labeling kit (Boehringer Mannheim). Unincorporated label was removed using MicroSpin S300-HR columns (Amersham Pharmacia Biotech). The RNA filter was then hybridized with fresh Church's Buffer containing labeled cDNA overnight, washed with 1X SCP (0.1 M NaCl, 0.03 M $Na_2HPO_4.7H_2O$, 0.001 M Na_2EDTA), 1% sarkosyl (n-lauroylsarcosine) and exposed to X-ray film.

Using both FACS and Northern analysis, P501S message and protein levels were found in increase in response to androgen treatment.

EXAMPLE 21

PREPARATION OF FUSION PROTEINS OF PROSTATE-SPECIFIC ANTIGENS

The example describes the preparation of a fusion protein of the prostate-specific antigen P703P and a truncated form of the known prostate antigen PSA. The truncated form of PSA has a 21 amino acid deletion around the active serine site. The expression construct for the fusion protein also has a restriction site at 3' end, immediately prior to the termination codon, to aid in adding cDNA for additional antigens.

The full-length cDNA for PSA was obtained by RT-PCR from a pool of RNA from human prostate tumor tissues using the primers of SEQ ID NO: 607 and 608, and cloned in the vector pCR-Blunt II-TOPO. The resulting cDNA was employed as a template to make two different fragments of PSA by PCR with two sets of primers (SEQ ID NO: 609 and 610; and SEQ ID NO: 611 and 612). The PCR products having the expected size were used as templates to make truncated forms of PSA by PCR with the primers of SEQ ID NO: 611 and 613, which generated PSA (delta 208-218 in amino acids). The cDNA for the mature form of P703P with a 6X histidine tag at the 5' end, was prepared by PCR with P703P and the primers of SEQ ID NO: 614 and 615. The cDNA for the fusion of P703P with the truncated form of PSA (referred to as FOPP) was then obtained by PCR using the modified P703P cDNA and the truncated form of PSA cDNA as templates and the primers of SEQ ID NO: 614 and 615. The FOPP

cDNA was cloned into the NdeI site and XhoI site of the expression vector pCRX1, and confirmed by DNA sequencing. The determined cDNA sequence for the fusion construct FOPP is provided in SEQ ID NO: 616, with the amino acid sequence being provided in SEQ ID NO: 617.

The fusion FOPP was expressed as a single recombinant protein in *E. coli* as follows. The expression plasmid pCRX1FOPP was transformed into the *E. coli* strain BL21-CodonPlus RIL. The transformant was shown to express FOPP protein upon induction with 1 mM IPTG. The culture of the corresponding expression clone was inoculated into 25 ml LB broth containing 50 ug/ml kanamycin and 34 ug/ml chloramphenicol, grown at 37 °C to OD600 of about 1, and stored at 4 °C overnight. The culture was diluted into 1 liter of TB LB containing 50 ug/ml kanamycin and 34 ug/ml chloramphenicol, and grown at 37 °C to OD600 of 0.4. IPTG was added to a final concentration of 1 mM, and the culture was incubated at 30 °C for 3 hours. The cells were pelleted by centrifugation at 5,000 RPM for 8 min. To purify the protein, the cell pellet was suspended in 25 ml of 10 mM Tris-Cl pH 8.0, 2mM PMSF, complete protease inhibitor and 15 ug lysozyme. The cells were lysed at 4 °C for 30 minutes, sonicated several times and the lysate centrifuged for 30 minutes at 10,000 x g. The precipitate, which contained the inclusion body, was washed twice with 10 mM Tris-Cl pH 8.0 and 1% CHAPS. The inclusion body was dissolved in 40 ml of 10 mM Tris-Cl pH 8.0, 100 mM sodium phosphate and 8 M urea. The solution was bound to 8 ml Ni-NTA (Qiagen) for one hour at room temperature. The mixture was poured into a 25 ml column and washed with 50 ml of 10 mM Tris-Cl pH 6.3, 100 mM sodium phosphate, 0.5% DOC and 8M urea. The bound protein was eluted with 350 mM imidazole, 10 mM Tris-Cl pH 8.0, 100 mM sodium phosphate and 8 M urea. The fractions containing FOPP proteins were combined and dialyzed extensively against 10 mM Tris-Cl pH 4.6, aliquoted and stored at - 70 °C.

EXAMPLE 22

REAL-TIME PCR CHARACTERIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S IN PERIPHERAL BLOOD OF PROSTATE CANCER PATIENTS

Circulating epithelial cells were isolated from fresh blood of normal individuals and metastatic prostate cancer patients, mRNA isolated and cDNA prepared using real-time PCR procedures. Real-time PCR was performed with the Taqman™ procedure using both gene specific primers and probes to determine the levels of gene expression.

Epithelial cells were enriched from blood samples using an immunomagnetic bead separation method (Dynal A.S., Oslo, Norway). Isolated cells were lysed and the magnetic beads removed. The lysate was then processed for poly A+ mRNA isolation using magnetic beads coated with Oligo(dT)25. After washing the beads in buffer, bead/poly A+ RNA samples were suspended in 10 mM Tris HCl pH 8.0 and subjected to reversed transcription. The resulting cDNA was subjected to real-time PCR using gene specific primers. Beta-actin content was also determined and used for normalization. Samples with P501S copies greater than the mean of the normal samples + 3 standard deviations were considered positive. Real time PCR on blood samples was performed using the Taqman™ procedure but extending to 50 cycles using forward and reverse primers and probes specific for P501S. Of the eight samples tested, 6 were positive for P501S and β-actin signal. The remaining 2 samples had no detectable β-actin or P501S. No P501S signal was observed in the four normal blood samples tested.

EXAMPLE 23

EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGENS P703P AND P501S IN SCID MOUSE-PASSAGED PROSTATE TUMORS

When considering the effectiveness of antigens in the treatment of prostate cancer, the continued presence of the antigens in tumors during androgen

ablation therapy is important. The presence of the prostate-specific antigens P703P and P501S in prostate tumor samples grown in SCID mice in the presence of testosterone was evaluated as follows.

Two prostate tumors that had metastasized to the bone were removed from patients, implanted into SCID mice and grown in the presence of testosterone. Tumors were evaluated for mRNA expression of P703P, P501S and PSA using quantitative real time PCR with the SYBR green assay method. Expression of P703P and P501S in a prostate tumor was used as a positive control and the absence in normal intestine and normal heart as negative controls. In both cases, the specific mRNA was present in late passage tumors. Since the bone metastases were grown in the presence of testosterone, this implies that the presence of these genes would not be lost during androgen ablation therapy.

EXAMPLE 24

ANTI-P503S MONOCLONAL ANTIBODY INHIBITS TUMOR GROWTH *IN VIVO*

The ability of the anti-P503S monoclonal antibody 20D4 to suppress tumor formation in mice was examined as follows.

Ten SCID mice were injected subcutaneously with HEK293 cells that expressed P503S. Five mice received 150 micrograms of 20D4 intravenously at day 0 (time of tumor cell injection), day 5 and day 9. Tumor size was measured for 50 days. Of the five animals that received no 20D4, three formed detectable tumors after about 2 weeks which continued to enlarge throughout the study. In contrast, none of the five mice that received 20D4 formed tumors. These results demonstrate that the anti-P503S Mab 20D4 displays potent anti-tumor activity *in vivo*.

EXAMPLE 25

CHARACTERIZATION OF A T CELL RECEPTOR CLONE FROM A P501S-SPECIFIC T CELL CLONE

T cells have a limited lifespan. However, cloning of T cell receptor (TCR) chains and subsequent transfer essentially enables infinite propagation of the T

cell specificity. Cloning of tumor-antigen TCR chains allows the transfer of the specificity into T cells isolated from patients that share the TCR MHC-restricting allele. Such T cells could then be expanded and used in adoptive transfer settings to introduce the tumor antigen specificity into patients carrying tumors that express the antigen. T cell receptor alpha and beta chains from a CD8 T cell clone specific for the prostate-specific antigen P501S were isolated and sequenced as follows.

Total mRNA from 2 x 10^6 cells from CTL clone 4E5 (described above in Example 12) was isolated using Trizol reagent and cDNA was synthesized. To determine Va and Vb sequences in this clone, a panel of Va and Vb subtype-specific primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of the clones expressed a common Vb sequence that corresponded to the Vb7 subfamily. Futhermore, using cDNA generated from the clone, the Va sequence expressed was determined to be Va6. To clone the full TCR alpha and beta chains from clone 4E5, primers were designed that spanned the initiator and terminator-coding TCR nucleotides. The primers were as follows: TCR Valpha-6 5'(sense): GGATCC---GCCGCCACC---ATGTCACTTTCTAGCCTGCT (SEQ ID NO: 899) BamHI site Kozak TCR alpha sequence TCR alpha 3' (antisense): GTCGAC---TCAGCTGGACCACAGCCGCAG (SEQ ID NO: 900) SalI site TCR alpha constant sequence TCR Vbeta-7. 5'(sense): GGATCC---GCCGCCACC--ATGGGCTGCAGGCTGCTCT (SEQ ID NO: 901) BamHI site Kozak TCR alpha sequence TCR beta 3' (antisense): GTCGAC---TCAGAAATCCTTTCTCTTGAC (SEQ ID NO: 902) SalI site TCR beta constant sequence. Standard 35 cycle RT-PCR reactions were established using cDNA synthesized from the CTL clone and the above primers, employing the proofreading thermostable polymerase PWO (Roche, Nutley, NJ).

The resultant specific bands (approx. 850 bp for alpha and approx. 950 for beta) were ligated into the PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E .coli* transformed with plasmids containing full-length alpha and beta chains were identified, and large scale preparations of the corresponding plasmids were generated. Plasmids containing full-length TCR alpha and beta chains were submitted

for sequencing. The sequencing reactions demonstrated the cloning of full-length TCR alpha and beta chains with the determined cDNA sequences for the Vb and Va chains being shown in SEQ ID NO: 903 and 904, respectively. The corresponding amino acid sequences are shown in SEQ ID NO: 905 and 906, respectively. The Va sequence was shown by nucleotide sequence alignment to be 99% identical (347/348) to Va6.2, and the Vb to be 99% identical to Vb7 (336/338).

EXAMPLE 26

CAPTURE OF PROSTATE SPECIFIC CELLS USING THE PROSTATE ANTIGEN P503S

As described above, P503S is found on the surface of prostate cells. Secondary coated microsphere beads specific for mouse IgG were coupled with the purified P503S-specific monoclonal antibody 1D12. The bound P503S antibody was then used to capture HEK cells expressing recombinant P503S. This provides a model system for prostate-specific cell capture which may be usefully employed in the detection of prostate cells in blood, and therefore in the detection of prostate cancer.

P503S-transfected HEK cells were harvested and redissolved in wash buffer (PBS, 0.1% BSA, 0.6% sodium citrate) at an appropriate volume to give at least 5^4 cells per sample. Round bottom Eppendorf tubes were used for all procedures involving beads. The stock concentrations were as shown below in Table VIII.

Table VIII

Stock concentrations	Sample concentration	Amount needed
Epithelial enrich beads 4^8 beads/ml (Dynal Biotech Inc. Lake Success, NY)	1^7 beads/ml	125 ul stock per 5 ml volume
1D12 ascites antibody 2 mg/ml	0.1 ug/ml (0.1X) to 5 ug/ml (5X) titrations	0.05 ul to 2.5 ul stock per sample
α- Mamma Mu 0.9 mg/ml	1 ug/ml (1X)	1.1 ul stock per sample
Pan-mouse IgG beads 4^8 beads/ml (Dynal Biotech)	1^7 beads/ml	125 ul stock per 5 ml volume

Blocked immunomagnetic beads were pre-washed as follows: all beads needed were pooled and washed once with 1 ml wash buffer. The beads were resuspended din a 3X volume of 1% BSA (v/v) in wash buffer and incubated for 15 min rotating at 4 °C. The beads were then washed three times with 2X volume of wash buffer and resuspended to original volume. Non-blocked beads were pooled, washed three times with 2X volume of wash buffer and resuspended to original volume.

Primary antibody was incubated with secondary beads in a fresh Eppendorf for 30 minutes, rotating at 4 °C. Approximately 200 ul wash buffer was added to increase the total volume for even mixing of the sample. The antibody-bead solution was transferred to a fresh Eppendorf, washed twice with an equal volume of wash buffer and resuspended to original volume. Target cells were added to each sample and incubated for 45 minutes, rotating at 4 °C. The tubes were transferred to a magnet, the supernatant removed, taking care not the agitate the beads, and the samples were washed twice with 1 ml wash buffer. The samples were then ready for RT-PCR using a Dynabeads mRNA direct microkit (Dynal Biotech).

Epithelial cell enrichment was placed in a magnet and supernant was removed. The epithelial enrichment beads were then resuspendedin 100 ul lysis/binding buffer fortified with Rnasin (2 U/ul per sample), and sotred at −70 °C until use. Oligo (dT_{25}) Dynabeads were pre-washed as follows: all beads needed were pooled (23 ul/sample), washed three times with an excess volume of lysis/binding buffer, and resuspended ot original volume. The lysis supernant was separated with a magnet and transferred to a fresh Eppendorf. 20 ul oligo(dT25) Dynabeads were added per samplem ad rolled for 5 min at room temperature. Supernant was separated using a magnet and discarded, leaving the mRNA annealed ot the beads. The bead/mRNA complex was washed with buffer and resuspended in cold Tris-HCl.

For RT-PCR, the Tris-HCl supernatant was separated and discarded using MPS. For each sample containing 1^5 cells or less, the following was added to give a total volume of 30 ul: 14.25 ul H_2O; 1.5 ul BSA; 6 ul first strand buffer; 0.75 mL 10 mM dNTP mix; 3 ul Rnasin; 3 ul 0.1M dTT; and 1.5 ul Superscript II. The resulting solution was incubated for 1 hour at 42 °C, diluted 1:5 in H2O, heated at 80°C for 2 min

to detach cDNA from the beads, and immediately placed on MPS. The supernatant containing cDNA was transferred to a new tube and stored at –20 °C.

Table IX shows the percentage of capture of P503S-transfected HEK cells as determined by RT-PCR.

Table IX

	% capture P503S-transfected HEK cells	% capture LnCAP cells
0.1 ug/ml P503S Mab	36.90	0.00
0.5 ug/ml P503S Mab	67.40	2.93
1 ug/ml P503S Mab	40.22	0.00
5 ug/ml P503S Mab	13.11	0.00
Anti-Mu beads only, non-blocked	1.42	0.00
Anti-Mu beads only, blocked	15.65	20.21
Absolute control, non-capture cells	100.00	100.00

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942 under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(b) sequences having at least 70% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(c) sequences having at least 90% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(d) sequences encoded by a polynucleotide of claim 1;

(e) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and

(f) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4. A host cell transformed or transfected with an expression vector according to claim 3.

5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6. A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7. A fusion protein comprising at least one polypeptide according to claim 2.

8. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,

593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942 under moderately stringent conditions.

9. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides according to claim 2;

(b) polynucleotides according to claim 1; and

(c) antigen-presenting cells that express a polypeptide according to claim 2,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

10. An isolated T cell population, comprising T cells prepared according to the method of claim 9.

11. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

(a) polypeptides according to claim 2;

(b) polynucleotides according to claim 1;

(c) antibodies according to claim 5;

(d) fusion proteins according to claim 7;

(e) T cell populations according to claim 10; and

(f) antigen presenting cells that express a polypeptide according to claim 2.

12. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 11.

13. A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 11.

14. A method for determining the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with an oligonucleotide according to claim 8;

(c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

15. A diagnostic kit comprising at least one oligonucleotide according to claim 8.

16. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

17. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate;

(b) administering to the patient an effective amount of the proliferated T cells,

and thereby inhibiting the development of a cancer in the patient.

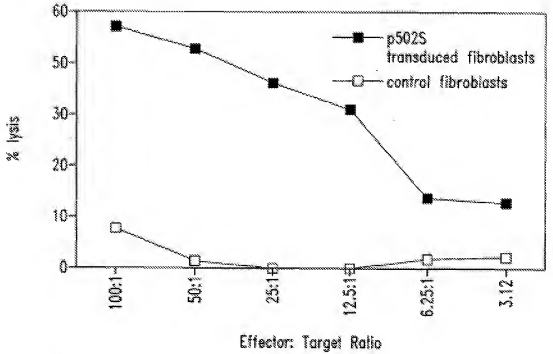

60
50
30
20
10
0
% lysis
p502S
transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

Fig. 1

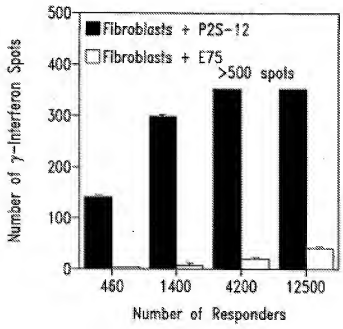

Fibroblasts + P2S-12
Fibroblasts + E75
>500 spots
Number of γ-Interferon Spots
500
400
300
200
100
0
460
1400
4200
12500
Number of Responders

Fig. 2A

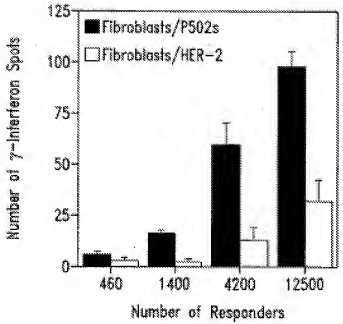

Fibroblasts/P502s
Fibroblasts/HER-2
Number of γ-Interferon Spots
125
100
75
50
25
0
460
1400
4200
12500
Number of Responders

Fig. 2B

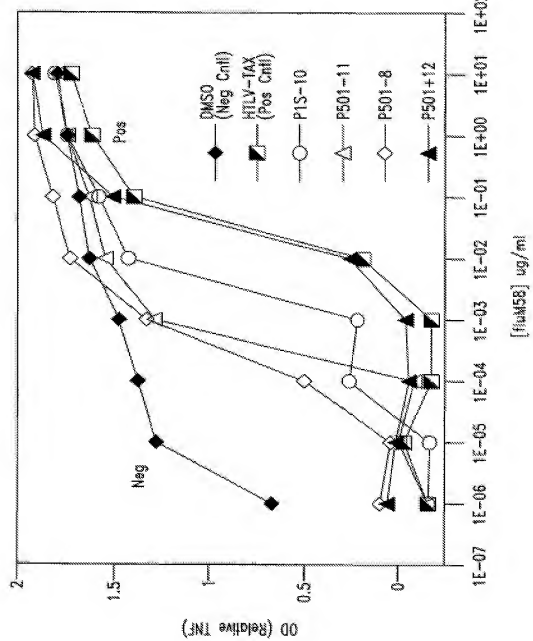

OD (Relative TNF)
2
1.5
1
0.5
0
Neg
Pos
DMSO (Neg Cntl)
HTLV-TAX (Pos Cntl)
P1S-10
P501-11
P501-8
P501+12
1E-07
1E-06
1E-05
1E-04
1E-03
1E-02
1E-01
1E+00
1E+01
1E+02
[flu/M58] ug/ml

Fig. 3

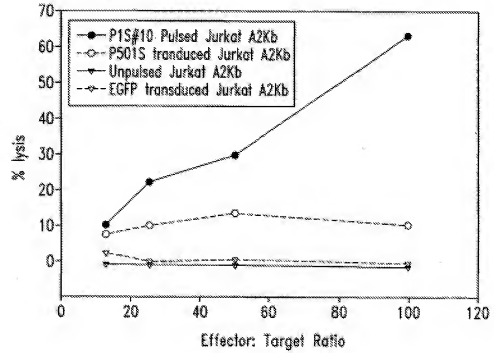

P1S#10 Pulsed Jurkat A2Kb
P501S transduced Jurkat A2Kb
Unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
Effector: Target Ratio
0
10
20
30
40
50
60
70
0
20
40
60
80
100
120

Fig. 4

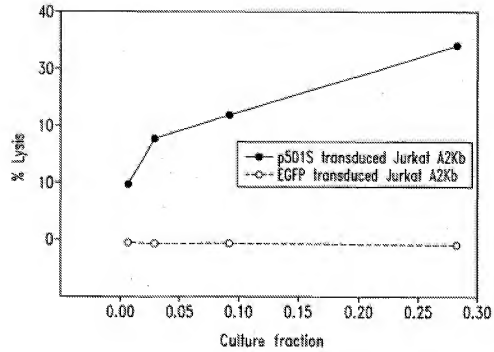

p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% Lysis
Culture fraction
0
10
10
30
40
0.00
0.05
0.10
0.15
0.20
0.25
0.30

Fig. 5

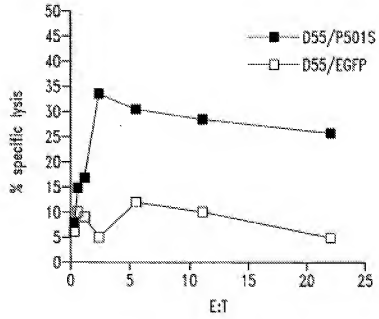

D55/P501S
D55/EGFP
% specific lysis
E:T
0
5
10
15
20
25
30
35
40
45
50

Fig. 6A

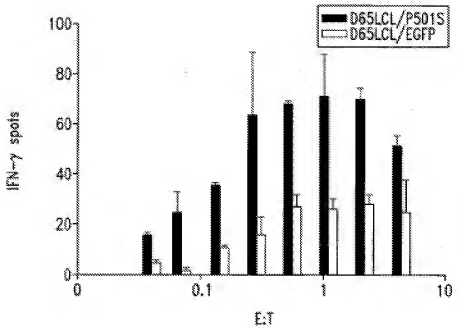
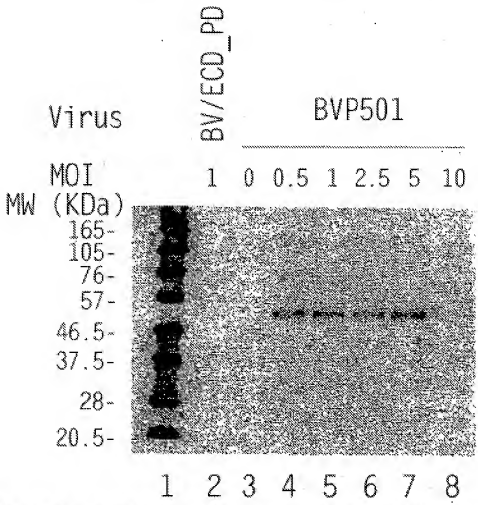

D65LCL/P501S
D65LCL/EGFP
IFN-γ spots
E:T
0
20
40
60
80
100
0.1
1
10

Fig. 6B

Expression of P501S
by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane2), without virus (lane3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

FIGURE 8. Mapping of the epitope recognized by 10E3-G4-D3

Fig. 8

Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT YVPPLLLEVGVEEKFM
TMVLGIGPVLGLVCYPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI DWDTSALAPYLGTQEE

CLFGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF VGEGLYQGVPRAEPGTEARRHYDEGVR

MGSLGLFLQCAISLVFSLVM *DRLVQRFGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA SAA

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF MGSIVQLSQS

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady an I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283. 489-506.

Fig. 9

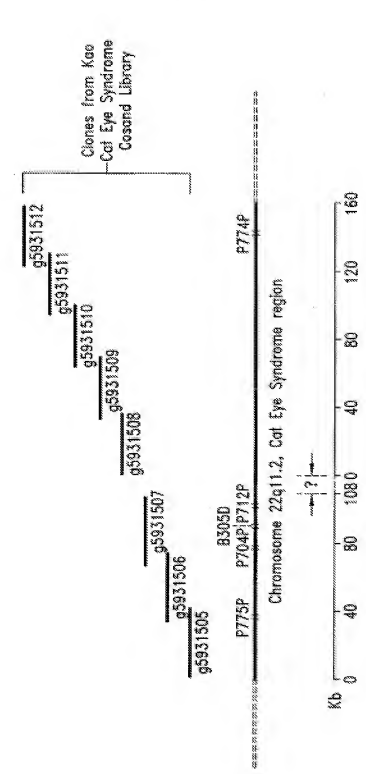

Genomic Map of (5) Corixa Candidate Genes
Clones from Kao Cat Eye Syndrome Cosand Library
g5931512
g5931511
g5931510
g5931509
g5931508
g5931507
g5931506
g5931505
B3050
P775P
P704P
P712P
P774P
Chromosome 22q11.2, Cat Eye Syndrome region
?
?
Kb
0
40
80
108 0
40
80
120
160

Fig. 10

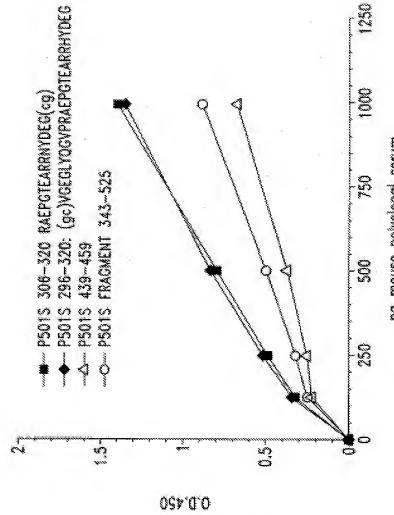

Elisa assay of rabbit polyclonal antibody specificity
P501S 306-320 RAEPGTEARRNYDEG(cg)
P501S 296-320: (gc)YDEGLYQGVPRAEPGTEARRHYDEG
P501S 439-459
P501S FRAGMENT 343-525
O.D.450
ng mouse polyclonal serum
0
0.5
1
1.5
2
0
250
500
750
1000
1250

Fig. 11

GTCACTTAGG AAAAGGTGTC CTTTCGGGCA GCCGGGCTCA GCATGAGGAA CAGAAGGAAT 60
GACACTCTGG ACAGCACCCG GACCCTGTAC TCCAGCGCGT CTCGGAGCAC AGACTTGTCT 120
TACAGTGAAA GCGACTTGGT GAATTTTATT CAAGCAAATT TTAAGAAACG AGAATGTGTC 180
TTCTTTACCA AAGATTCCAA GGCCACGGAG AATGTGTGCA AGTGTGGCTA TGCCCAGAGC 240
CAGCACATGG AAGGCACCCA GATCAACCAA AGTGAGAAAT GGAACTACAA GAAACACACC 300
AAGGAATTTC CTACCGACGC CTTTGGGGAT ATTCAGTTTG AGACACTGGG GAAGAAAGGG 360
AAGTATATAC GTCTGTCCTG CGACACGGAC GCGGAAATCC TTTACGAGCT GCTGACCCAG 420
CACTGGCACC TGAAAACACC CAACCTGGTC ATTTCTGTGA CCGGGGGCGC CAAGAACTTC 480
GCCCTGAAGC CGCGCATGCG CAAGATCTTC AGCCGGCTCA TCTACATCGC GCAGTCCAAA 540
GGTGCTTGGA TTCTCACGGG AGGCACCCAT TATGGCCTGA CGAAGTACAT CGGGGAGGTG 600
GTGAGAGATA ACACCATCAG CAGGAGTTCA GAGGAGAATA TTGTGGCCAT TGGCATAGCA 660
GCTTGGGGCA TGGTCTCCAA CCGGGACACC CTCATCAGGA ATTGCGATGC TGAGGGCTAT 720
TTTTTAGCCC AGTACCTTAT GGATGACTTC ACAAGGGATC CACTGTATAT CCTGGACAAC 780
AACCACACAC ATTTGCTGCT CGTGGACAAT GGCTGTCATG GACATCCCAC TGTCGAAGCA 840
AAGCTCCGGA ATCAGCTAGA GAAGCATATC TCTGAGCGCA CTATTCAAGA TTCCAACTAT 900
GGTGGCAAGA TCCCCATTGT GTGTTTTGCC CAAGGAGGTG GAAAAGAGAC TTTGAAAGCC 960
ATCAATACCT CCATCAAAAA TAAAATTCCT TGTGTGGTGG TGGAAGGCTC GGGCCGGATC 1020
GCTGATGTGA TCGCTAGCCT GGTGGAGGTG GAGGATGCCC CGACATCTTC TGCCGTCAAG 1080
GAGAAGCTGG TGCGCTTTTT ACCCCGCACG GTGTCCCGGC TGTCTGAGGA GGAGACTGAG 1140
AGTTGGATCA AATGGCTCAA AGAAATTCTC GAATGTTCTC ACCTATTAAC AGTTATTAAA 1200
ATGGAAGAAG CTGGGGATGA AATTGTGAGC AATGCCATCT CCTACGCTCT ATACAAAGCC 1260
TTCAGCACCA GTGAGCAAGA CAAGGATAAC TGGAATGGGC AGCTGAAGCT TCTGCTGGAG 1320
TGGAACCAGC TGGACTTAGC CAATGATGAG ATTTTCACCA ATGACCGCCG ATGGGAGTCT 1380
GCTGACCTTC AAGAAGTCAT GTTTACGGCT CTCATAAAGG ACAGACCCAA GTTTGTCCGC 1440
CTCTTTCTGG AGAATGGCTT GAACCTACGG AAGTTTCTCA CCCATGATGT CCTCACTGAA 1500
CTCTTCTCCA ACCACTTCAG CACGCTTGTG TACCGGAATC TGCAGATCGC CAAGAATTCC 1560
TATAATGATG CCCTCCTCAC GTTTGTCTGG AAACTGGTTG CGAACTTCCG AAGAGGCTTC 1620
CGGAAGGAAG ACAGAAATGG CCGGGACGAG ATGGACATAG AACTCCACGA CGTGTCTCCT 1680
ATTACTCGGC ACCCCCTGCA AGCTCTCTTC ATCTGGGCCA TTCTTCAGAA TAAGAAGGAA 1740
CTCTCCAAAG TCATTTGGGA GCAGACCAGG GGCTGCACTC TGGCAGCCCT GGGAGCCAGC 1800
AAGCTTCTGA AGACTCTGGC CAAAGTGAAG AACGACATCA ATGCTGCTGG GGAGTCCGAG 1860
GAGCTGGCTA ATGAGTACGA GACCCGGGCT GTTGAGCTGT TCACTGAGTG TTACAGCAGC 1920
GATGAAGACT TGGCAGAACA GCTGCTGGTC TATTCCTGTG AAGCTTGGGG TGGAAGCAAC 1980
TGTCTGGAGC TGGCGGTGGA GGCCACAGAC CAGCATTTCA CCGCCCAGCC TGGGGTCCAG 2040
AATTTTCTTT CTAAGCAATG GTATGGAGAG ATTTCCCGAG ACACCAAGAA CTGGAAGATT 2100

Fig. 12A (1)

ATCCTGTGTC TGTTTATTAT ACCCTTGGTG GGCTGTGGCT TTGTATCATT TAGGAAGAAA 2160
CCTGTCGACA AGCACAAGAA GCTGCTTTGG TACTATGTGG CGTTCTTCAC CTCCCCCTTC 2220
GTGGTCTTCT CCTGGAATGT GGTCTTCTAC ATCGCCTTCC TCCTGCTGTT TGCCTACGTG 2280
CTGCTCATGG ATTTCCATTC GGTGCCACAC CCCCCGAGC TGGTCCTGTA CTCGCTGGTC 2340
TTTGTCCTCT TCTGTGATGA AGTGAGACAG TGGTACGTAA ATGGGGTGAA TTATTTTACT 2400
GACCTGTGGA ATGTGATGGA CACGCTGGGG CTTTTTTACT TCATAGCAGG AATTGTATTT 2460
CGGCTCCACT CTTCTAATAA AAGCTCTTTG TATTCTGGAC GAGTCATTTT CTGTCTGGAC 2520
TACATTATTT TCACTCTAAG ATTGATCCAC ATTTTTACTG TAAGCAGAAA CTTAGGACCC 2580
AAGATTATAA TGCTGCAGAG GATGCTGATC GATGTGTTCT TCTTCCTGTT CCTCTTTGGG 2640
GTGTGGATGG TGGCCTTTGG CGTGGCCAGG CAAGGGATCC TTAGGCAGAA TGAGCAGCGC 2700
TGGAGGTGGA TATTCCGTTC GGTCATCTAC GAGCCCTACC TGGCCATGTT CGGCCAGGTG 2760
CCCAGTGACG TGGATGGTAC CACGTATGAC TTTGCCCACT GCACCTTCAC TGGGAATGAG 2820
TCCAAGCCAC TGTGTGTGGA GCTGGATGAG CACAACCTGC CCCGGTTCCC CGAGTGGATC 2880
ACCATCCCCC TGGTGTGCAT CTACATGTTA TCCACCAACA TCCTGCTGGT CAACCTGCTG 2940
GTCGCCATGT TTGGCTACAC GGTGGGCACC GTCCAGGAGA ACAATGACCA GGTCTGGAAG 3000
TTCCAGAGGT ACTTCCTGGT GCAGGAGTAC TGCAGCCGCC TCAATATCCC CTTCCCCTTC 3060
ATCGTCTTCG CTTACTTCTA CATGGTGGTG AAGAAGTGCT TCAAGTGTTG CTGCAAGGAG 3120
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TTGATGAACA CATATATAGG AGAACATCTA TCCTATGAAT AAGAACCTGG TCATGCTTTA 3720
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GAATCCTATT GCTGTATTTG GGAAAATTTT CCAAGGTTAG ATTCCAATAA ATATCTATTT 4500
ATTATTAAAT ATTAAAATAT CGATTTATTA TTAAAACCAT TTATAAGGCT

Fig. 12A (2)

```
                                                                TTTTCATAAA 4560
TGTATAGCAA ATAGGAATTA TTAACTTGAG CATAAGATAT GAGATACATG AACCTGAACT 4620
ATTAAAATAA AATATTATAT TTAACCCTAG TTTAAGAAGA AGTCAATATG CTTATTTAAA 4680
TATTATGGAT GGTGGGCAGA TCACTTGAGG TCAGGAGTTC GAGACCAGCC TGGCCAACAT 4740
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TAATCCCAGC TACTCAGAAG GCTGAGGTAC AAGAATTGCT GGAACCTGGG AGGCGGAGGT 4860
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TGAAAATAAA TAAATAAATA AATAAATAAA TAAATAAATA AATATTATGG ATGGTGAAGG 4980
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AAAAGATCTA ATTTGAAAAA CTACAAAAGC ATTAACTAAA AAAGTTTATT TTCCTTTTGT 5220
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AAATAAATAA TGGAGGAATT GTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 5640
AAAAAAAAAA AAAAAAAAAA AAAAAAAA                                    5668
```

Fig. 12A (3)

MRNRRNDTLDSTRTLYSSASRSTDLSYSESDLVNFIQANFKKRECVFFTKDSKATENVCKCGYAQSQHME
GTQINQSEKWNYKKHTKEFPTDAFGDIQFETLGKKGKYIRLSCDTDAEILYELLTQHWHLKTPNLVISVT
GGAKNFALKPRMRKIFSRLIYIAQSKGAWILTGGTHYGLTKYIGEVVRDNTISRSSEENIVAIGIAAWGM
VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT
IQDSNYGGKIPIVCFAQGGGKETLKAINTSIKNKIPCVVVEGSGRIADVIASLVEVEDAPTSSAVKEKLV
RFLPRTVSRLSEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQDKDNWNGQ
LKLLLEWNQLDLANDEIFTNDRRWESADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFSN
HFSTLVYRNLQIAKNSYNDALLTFVWKLVANFRRGFRKEDRNGRDEMDIELHDVSPITRHPLQALFIWAI
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VSFRKKPVDKHKKLLWYYVAFFTSPFVVFSWNVVFYIAFLLLFAYVLLMDFHSVPHPPELVLYSLVFVLF
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Fig. 12B

SEQUENCE LISTING

<110> Corixa Corporation
Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Yuqui, Jiang
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William
Henderson, Robert A.

<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER

<130> 210121.42723PC

<140> PCT
<141> 2001-03-27

<160> 943

<170> FastSEQ for Windows Version 3.0

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<223> n = A,T,C or G

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aagtttgcag atgtatttgc aaagaagacg aaggcagagt ggtgtcaaat ctttgacggc 240
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gtgactggga aaaccctggg cgttaccaac ttaatcgcct tgcagcacat ccccctttcg 540
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<220>
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<223> n = A,T,C or G

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tcggaacact ggctgtctct gaagacttct cgctcagttt cagtgaggac acacacaaag     180
acgtgggtga ccatgttgtt tgtggggtgc agagatggga ggggtggggc ccaccctgga     240
agagtggaca gtgacacaag gtggacactc tctacagatc actgaggata agctggagcc     300
acaatgcatg aggcacacac acagcaagga tgacnctgta aacatagccc acgctgtcct     360
gnggggcactg ggaagcctan atnaggccgt gagcanaaag aaggggagga tccactagtt     420
ctanagcggc cgccaccgcg gtggagctcc ancttttgtt ccctttagtg agggttaatt     480
gcgcgcttgg cntaatcatg gtcatancta tttcctgtgt gaaattgtta tccgctcaca     540
attccacaca acatacgagc cggaagcata aantgtaaac ctggggtgcc taatgantga     600
ctaactcaca ttaattgcgt tgcgctcact gcccgctttc caatcnggaa acctgtcttg     660
ccncttgcat tnatgaatcn gccaaccccc ggggaaaagc gtttgcgttt tgggcgctct     720
tccgcttcct cnctcantta ntccctncnc tcggtcattc cggctgcngc aaaccggttc     780
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<213> Homo sapien

<220>
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attttataac aatcaacacc tgtggctttt aaaatttggt tttcataaga taatttatac     180
tgaagtaaat ctagccatgc ttttaaaaaa tgctttaggt cactccaagc ttggcagtta     240
acatttggca taaacaataa taaaacaatc acaatttaat aaataacaaa tacaacattg     300
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aatagaatac cttggcctct atgcaaatat gtctagacac tttgattcac tcagccctga     420
cattcagttt tcaaagtagg agacaggttc tacagtatca ttttacagtt tccaacacat     480
tgaaaacaag tagaaaatga tgagttgatt tttattaatg cattacatcc tcaagagtta     540
tcaccaaccc ctcagttata aaaaatttc aagttatatt agtcatataa cttggtgtgc     600
ttattttaaa ttagtgctaa atggattaag tgaagacaac aatggtcccc taatgtgatt     660
gatattggtc atttttacca gcttctaaat ctnaactttc aggcttttga actggaacat     720
tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa     780
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```

<210> 6
<211> 818
<212> DNA
<213> Homo sapien

<220>
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<223> n = A,T,C or G

<400> 6

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tgtaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagttg agccaataat     180
gacgtgaagt ccgtggaagc ctgtggctac aaaaaatgtt gagccgtaga tgccgtcgga     240
aatggtgaag ggagactcga agtactctga ggcttgtagg agggtaaaat agagacccag     300
taaaattgta ataagcagtg cttgaattat ttggtttcgg ttgttttcta ttagactatg     360
gtgagctcag gtgattgata ctcctgatgc gagtaatacg gatgtgttta ggagtgggac     420
ttctagggga tttagcgggg tgatgcctgt tgggggccag tgccctccta gttggggggt     480
aggggctagg ctggagtggt aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga     540
ggtaataaat aggattatcc cgtatcgaag gccttttgg acaggtggtg tgtggtggcc      600
ttggtatgtg ctttctcgtg ttacatcgcg ccatcattgg tatatggtta gtgtgttggg     660
ttantanggc ctantatgaa gaacttttgg antggaatta aatcaatngc ttggccggaa     720
gtcattangc nggctnaaaa ggccctgtta ngggtctggg ctnggtttta cccnacccat     780
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<210> 7
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<213> Homo sapien

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<400> 7

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ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcggtga     180
aagtggtttg gtttagacgt ccgggaattg catctgtttt taagcctaat gtggggacag     240
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gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tggttctagg aataatgggg     360
gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc     420
attggtggcc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa     480
aggatncctt ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangatatt     540
tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaan tttngttatt     600
gaatatttnng gaaaagggct tacaggacta gaaaccaaat angaaaanta atnntaangg    660
cnttatcnta aaaggtnata accnctccta tnatccccacc caatngnatt ccccacncnn    720
acnattggat nccccanttc canaaanggc cnccccccgg tgnannccnc cttttgttcc     780
cttnantgan ggttattcnc ccctngcatt atcancc                              817
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<223> n = A,T,C or G

<400> 8

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ctgaagcgca cgtcccagaa ggtggacttg gcactgaaac agctgggaca catccgcgag     180
tacgaacagc gcctgaaagt gctggagcgg gaggtccagc agtgtagccg cgtcctgggg     240
tgggtggccg angcctganc cgctctgcct tgctgccccc angtgggccg ccaccccctg     300
acctgcctgg gtccaaacac tgagccctgc tggcggactt caagganaac ccccacangg     360
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ggattttgct cctanantaa ggctcatctg ggcctcggcc ccccmacctg gttggccttg      420
tctttgangt gagccccatg tccatctggg ccactgtcag gaccaccttt ngggagtgtt      480
ctccttacaa ccacannatg cccggctcct cccggaaacc antcccancc tgngaaggat      540
caagncctgn atccactnnt nctanaaccg gccnccncog cngtggaacc cnccttntgt      600
tcctttttcnt tnagggttaa tnncgccttg gccttnccan ngtcctncnc nttttccnnt     660
gttnaaattg ttangcnccc nccnntcccn cnacnncnan cccgacccnn annttaaann      720
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caaggacaag gccaccaggt gcgggggccg aagcccacat gatccttact ctatgagcaa      180
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cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg      600
ttaaaaaatt ccagcaacat tggggtgga aggcctgcct cactgggtcc aactccccgc       660
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ggngttccc                                                              789

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      &lt;213&gt; Homo sapien

      &lt;220&gt;
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      &lt;223&gt; n = A,T,C or G

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accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc      180
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gcacagggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact ngggggggca      660
acccggccac cccnangggg gttaacngga ancngggnaa cntggaaccc aattnaggca      720
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      &lt;211&gt; 751
      &lt;212&gt; DNA
      &lt;213&gt; Homo sapien

      &lt;220&gt;
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      &lt;223&gt; n = A,T,C or G

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ttggctgtgt tggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg      180
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ggcactacca gcaacgtcag ggaagtgctc agccattgtg gtgtacacca aggcgaccac      360
agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc      420
acacttgctc tcagtcttan cacccatanca gcccntgaaa accaanaaca aagaccacna      480
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tnatnaacnt gaaccctgcn tngtggctcc tgttcaggnc cnnggcctga cttctnaann      720
aangaacten gaagnccccca cnggananne g                                    751

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      &lt;212&gt; DNA
      &lt;213&gt; Homo sapien
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ctgtgtggtg cagccctgtt ggcagtgggc atctgggtgt caatcgatgg ggcatccttt    240
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ctcatcgcag ccggcgttgt ggtctttgct ctaggtttcc tgggctgcta tggtgctaag    360
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gaggttgcaa tgctgtggtc gcctttggtgt acaccacaat ggctgagcac ttcctgacgt    480
tgctggtaat gcctgccatc aanaaaagat tatgggttcc caggaanact tcactcaagt    540
gttggaacac caccatgaaa gggctcaagt gctgtggctt cnnccaacta tacggatttt    600
gaagantcac ctacttcaaa gaaaanagtg cctttccccc atttctgttg caattgacca    660
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attcaaggg                                                            729
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<212> DNA
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<220>
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tgttcgctga aggggttgta gtaccagcgc gggatgctct ccttgcagag tcctgtgtct    120
ggcaggtcca cgcagtgccc tttgtcactg gggaaatgga tgcgctggag ctcgtcaaag    180
ccactcgtgt atttttcaca ggcagcctcg tccgacgcgt cggggcagtt ggggtgtct    240
tcacactcca ggaaactgtc natgcagcag ccattgctgc agcggaactg ggtgggctga    300
cangtgccag agcacactgg atggcgcctt tccatgnnan gggccctgng ggaaagtccc    360
tgancccccan anctgcctct caaangcccc accttgcaca ccccgacagg ctagaatgga    420
atcttcttcc cgaaaggtag ttnttcttgt tgcccaancc ancccentaa acaaactctt    480
gcanatctgc tccgnggggg tcntantacc ancgtgggaa aagaaccccca ggcngcgaac    540
caancttgtt tggatncgaa gcnataatct nctnttctgc ttggtggaca gcaccantna    600
ctgtnnanct ttagnccntg gtcctcntgg gttgnncttg aacctaatcn ccnntcaact    660
gggacaaggt aantngccnt cctttnaatt cccnancntn cccctggtt tggggttttn    720
cncnctccta ccccagaaan ncogtgttcc cccccaacta ggggccnaaa ccnntntte    780
cacaaccctn ccccacccac gggttcngnt ggttng                              816
```

<210> 15
<211> 783
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(783)
<223> n = A,T,C or G

<400> 15
```
ccaaggcctg ggcaggcata nacttgaagg tacaacccca ggaacccctg gtgctgaagg      60
```

atgtggaaaa cacagattgg cgcctactgc ggggtgacac ggatgtcagg gtagagagga 120
aagacccaaa ccaggtggaa ctgtggggac tcaaggaang cacctacctg ttccagctga 180
cagtgactag ctcagaccac ccagaggaca cggccaacgt cacagtcact gtgctgtcca 240
ccaagcagac agaagactac tgcctgcat ccaacaangt gggtcgctgc cggggctctt 300
tccacgctg gtactatgac cccacggagc agatctgcaa gagtttcgtt tatggaggct 360
gcttgggcaa caagaacaac tacctcggg aagaagagtg cattctancc tgtcngggtg 420
tgaaggtgg gcctttgana ngcanctctg gggctcangc gacttttccc dagggcccct 480
ccatggaaag gcgccatcca ntgttctctg gcacctgtca gcccanccag ttccgctgca 540
ncaatggctg ctgcatcnac antttcctng aattgtgaca acacccccca ntgccccccaa 600
cccttccaac aaagcttncc tgttnaaaaa tacnccantt ggcttttnac aaacnccgg 660
cncctccntt ttccccnntn aacaaagggc nctngcnttt gaactgcccn aaccchggaa 720
tctncnnngg aaaaantncc cccctggtt cctnnaancc cctccncnaa anctncccc 780
ccc 783

<210> 16
<211> 801
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)..(801)
<223> n = A,T/C or G

<400> 16
gcccaattc cagctgccac accacccacg gtgactgcat tagttcggat gtcatacaaa 60
agctgattga agcaacccta tacttttgg tcgtgagcct tttgcttggt gcaggtttca 120
ttggctgtgt tggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180
aagtagggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc 240
atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca 300
ggcactacca gcaacgtcag gaagtgctca gccattgtgg tgtacaccaa ggcgaccaca 360
gcagctgcaa cctcagcaat gaagatgagg aggaggatga agaagaacgt cncgagggca 420
cacttgctct ccgtcttagc accatagcag cccangaaac caagagcaaa gaccacaacg 480
ccngctgcga atgaaagaaa ntacccacgt tgacaaactg catggccact ggacgacagt 540
tggcccgaan atcttcagaa aagggatgcc cnatcgattg aacaccccna tgcccactgc 600
cnacagggct gcnccncncn gaaagaatga gccattgaag aaggatcntc ntggtcttaa 660
tgaactgaaa ccntgcatgg tggcccctgt tcagggctct tggcagtgaa ttctgannaa 720
aaggaacngc ntnagccccc ccaaangana aaacaccccc gggtgttgcc ctgaattggc 780
ggccaaggan ccctgcccnn g 801

<210> 17
<211> 740
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)..(740)
<223> n = A,T/C or G

<400> 17
gtgagagccn ggcgtcccctc tgcctgccca ctcagtggca acacccggga gctgttttgt 60
cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg 120
agccaccatg cagtgcttca gcttcattaa gaccatgatg atcctcttca atttgctcat 180
ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc 240
cttttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgtca acgtgggcta 300
cttcctcatc gcagccggcg ttgtggtctt tgctcttggt ttcctgggct gctatggtgc 360
taagacggag agcaagtgtg ccctcgtgac gttcttcttc atcatcctcc tcatcttcat 420

```
tgctgaagtt gcagctgctg tggtcgcctt ggtgtacacc acaatggctg aaccattcct      480
gacgttgctg gtantgcctg ccatcaanaa agattatggg ttcccaggaa aaattcactc      540
aantntggaa cacccnccatg aaaagggctc caatttctgn tggcttcccc aactatacccg      600
gaattttgaa agantcnccc tactttcaaa aaaaaanant tgcctttncc cccnttctgt      660
tgcaatgaaa acntcccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa      720
caaaaaaant nnaagggttn                                                   740

      <210> 18
      <211> 802
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(802)
      <223> n = A,T,C or G

      <400> 18
ccgctggttg cgctggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca       60
caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg      120
ggatacactt tactttagca gccagggtga caactgagag gtgtcgaagc ttattcttct      180
gagcctctgt tagtggagga agattccggg cttcagctaa gtagtcagcg tatgtcccat      240
aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa      300
cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat      360
ggatgagtgt ggccagcgct gccccttgg ccgacttggc taggagcaga aattgctcct      420
ggttctgccc tgtcaccttc acttccgcac tcatcactgc actgagtgtg gggacttgg       480
gctcaggatg tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc      540
gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgctggc cnctacttgc      600
aancttcgtc nggcccatgg aattcaccnc accggaactn gtangatcca ctnattctat      660
aaccggncgc caccgcnnnt ggaactccac tcttnttncc tttacttgag ggttaaggtc      720
accctttnncg ttaccttggt ccaaaccntn ccntgtgtcg anatngtnaa tcnggnccna      780
tnccancenc atangaagcc ng                                                802

      <210> 19
      <211> 731
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(731)
      <223> n = A,T,C or G

      <400> 19
cnaagcttcc aggtaacggg ccgcnaancc tgacccnagg tancanaanq cagncgcgg        60
gagcccaccg tcacgnaggng gngtctttat nggaggggc ggagcccacat cnctggccnt      120
cntgaccccca actccccncc ncncantgca gtgatgagtg cagaactgaa ggtnacgtgg      180
caggaaccaa gancaaannc tgctccnntc caagtcggcn naggggcgg ggctggccac       240
gcncatccnt cnagtgctgn aaagccccnn cctgtctact tgtttggaga acngcnnaga      300
catgcccagn gttaaataac nggcngagag tnantttgcc tctcccttcc ggctgcgcan      360
cgngtatgct tagnggacat aacctgacta cttaactgaa cccnngaatc tngcnccccct      420
ccactaagct cagaacaaaa aacttcgaca ccactcaatt gtcacctgnc tgctcaagta      480
aagtgtaccc catncccaat gtntgctnga ngctctgncc tgcnttangt tcggtcctgg      540
gaagacctat caattnaagc tatgtttctg actgcctctt gctccctgna acaancnacc      600
cnncnntcca agggggggnc ggccccccaat cccccaacc ntnaattnan tttancccn       660
ccccnggcc cggcctttta cnancntcnn nnacnggna aaacennngc tttnccccaac       720
nnaatccncc t                                                            731
```

<210> 20
<211> 754
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(754)
<223> n = A,T,C or G

<400> 20
tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60
caacccccta ntccaaatnn ccntttccgg gnggggcttc caaacccaan ttanntttgg 120
annttaaatt aaatnttnnt tggnggnnna anccnaatgt nangaaagtt naacccanta 180
tnancttnaa tncctggaaa ccngtngatt ccaaaaatnt ttaaccctta antccctccg 240
aaatngttna nggaaaaccc aanttctcnt aaggttgttt gaaggntnaa tnaaaanccc 300
nnccaattgt ttttngccac gcctgaatta attggnttcc gntgttttcc nttaaaanaa 360
ggnnaacccc ggttantnaa tccccccnnc cccaattata ccgantttttt ttngaattgg 420
ganccccncgg gaattaacgg ggnnnntccc tnttgggggg cnggnnccoc ccccntcggg 480
ggttngggnc aggncnnaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc 540
ccaggntgag nntngggttt nccccccccc canggcccct ctcgnanagt tggggtttgg 600
ggggcctggg attttntttc ccctnttncc tccccccccc ccngggganag aggttngngt 660
tttgntcnnc ggccccnccn aagancttttn ccgantttnan ttaaatccnt gcctnggcga 720
agtccnttgn agggntaaan ggcccccctnn cggg 754

<210> 21
<211> 755
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(755)
<223> n = A,T,C or G

<400> 21
atcanoccat gaccccnaac nngggaccnc tcancoggnc nnacnaccnc cggccnatca 60
nngtnagnnc actncnnttn natcacnccc cnccnactac gcccncnanc cnacgcncta 120
nncanatncc actgannqcg cganqtngan ngagaaanct natacccanag ncaccanacn 180
ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnancctc cnaagtattn 240
nncnncanat gattttcctn ancogattac ccntnccccc tanccccctcc ccccaacna 300
cgaaggcnct ggnccnaagg nngcgncncc ccgctagntc cccnncaagt cncncncccta 360
aactcanccn nattacncgc ttcntgagta tcactccccg aatctcaccc tactcaactc 420
aaaaanatcn gatacaaaat aatncaagcc tgnttatnac actntgactg ggtctctatt 480
ttagnggtcc ntnaancatc ctaatacttc cagtctncct tcnccaattt ccnaangget 540
ctttcngaca gcatnttttg gttcccnntt gggttcttan ngaattgccc ttcntngaac 600
gggctcntct tttccttcgg ttancctggn ttcnncoggc cagttattat ttcccntttt 660
aaattcctnc cntttantttt tggcnttcna aaccccoggc cttgaaaacg gcccccctggt 720
aaaaggttgt tttganaaaa tttttgtttt gttcc 755

<210> 22
<211> 849
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(849)

<223> n = A,T,C or G

<400> 22
tttttttttt tttttangtg tngtcgtgca ggtagaggct tactacaant gtgaanacgt 60
acgctnggan taangcgacc cganttctag gaancnccct aaaatcanac tgtgaagatn 120
atcctgnnna cggaanggtc acgggnngat nntgctaggg tgnccnctcc cannncnttn 180
cataactcng nggccctgcc caccaccttc ggcggcccng ngnccgggcc cgggtcattn 240
gnnttaaccn cactnngcna ncggtttccn nccccnncng acccnggcga tccggggtnc 300
tctgtcttcc cctgnagncn anaaantggg cncggncccc ctttacccct nnacaagcca 360
cngccntcta nccncngccc cccctccant nngggggact gccnanngct ccgttnctng 420
nnaccccnnn gggtncctcg gttgtcgant cnaccgnang ccanggattc cnaaggaagg 480
tgcgttnttg gcccctaccc ttcgctncgg nncacccttc ccgacnanga nccgctcccg 540
cncnncgnng cctcncctcg caacacccgc nctcntcngt ncggnnnccc cccnacccgc 600
nccctcncnc ngncgnancn ctccnccncc gtctcannca ccaccccgcc ccgccaggcc 660
ntcanccacn ggnngacnng nagcncnntc gcnccgcgcn gcgncnccct cgccncngaa 720
ctacntcngg ccantnncgc tcaanccnna cnaaacgccg ctgcgcggcc cgnagcgncc 780
ncctccncga gtcctcccgn cttccnaccc angnnttcca cgaggacacn nnacccagcc 840
nncangcgg 849

<210> 23
<211> 872
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(872)
<223> n = A,T,C or G

<400> 23
gcgcaaacta tacttcgctc gnactcgtgc gcctcgctnc tcttttcctc cgcaaccatg 60
tctgacaanc ccgattnggc ngatatcnan aagntcganc agtccaaact gantaacaca 120
cacacncnan agananatcc nctgccttcc anagtanacn attgaacnng agaaccangc 180
nggcgaatcg taatnaggcg tgcgccgcca atntgtcncc gtttattntn ccagcntcnc 240
ctnccnaccc tacntcttcn nagctgtcnn acccctngtn cgnacccccc naggtcggga 300
tcgggtttan nntgaccgng cnncccctcc cccnntccat nacganccnc ccgcaccacc 360
nanngcncgc nccccgnact cttcgccncc ctgtcctntn cccctgtngc ctggcncngn 420
accgcattga ccctcgccnn ctncnngaaa ncgnanacgt ccgggttgnn nnnancgctg 480
tgggnnngcg tctgcnccgc gttccttccn ncnncttcca ccatcttcnt tacngggtct 540
ccacgccntc tcnnncacnc cctgggacgc tntcctntgc cccccttnac tccccccctt 600
cgncgtgncc cgnccccacc ntcatttnca nacgntcttc acaannncct ggntnnctcc 660
cnancngncn gtcanccnag ggaagggngg ggnnccnntg nttgacgttg nggngangtc 720
cgaanantcc tcnccntcan cnctacccct cgggcgnnct ctcngttncc aacttancaa 780
ntctcnnccg ngngcacntc tcagcctcnc ccnccccnct ctctgcantg tnctctgctc 840
tnaccnntac gantattcgn cnccctcttt cc 872

<210> 24
<211> 815
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(815)
<223> n = A,T,C or G

<400> 24
gcatgcaagc ttgagtattc tatagngtca cctaaatanc ttggcntaat catggtcnta 60

```
nctgnettcc tgtgtcaaat gtatacnaan tanatatgaa tctnatntga caagannnta      120
tcntncatta gtaacaantg tnntgtccat cctgtcngan canattccca tnnattncgn      180
cgcattcncn gcncantatn taatngggaa ntcnnntnnn ncaccnncat ctatcntncc      240
gcncccctgac tggnagagat ggatnaattc tnntatgacc nacatgttca tcttggattn     300
aananccccc cgcngnccac cggttagnng cnagccnntc ccaagacctc ctgtggaggt      360
aacctgcgtc aganncatca aacntgggaa acccgcnncc angtnnaagt ngnnncanan      420
gatcccgtcc aggnttnacc atcccttcnc agcgccccct ttagtgcctt anagngnagc      480
gtgtccnanc cnctcaacat ganacgcgcc agnccanccg caattnggca caatgtcgnc      540
gaaccccccta gggggantna tncaaancc caggattgtc cncncangaa atcccncanc      600
cccncccctac ccnnctttgg gacngtgacc aantccccgga gtnccagtcc ggccngnctc   660
cnccaccggt nnccntgggg gggtgaanct cngnntcanc cngncgaggn ntcgnaagga      720
accggnnctn ggncgaanng ancnntcnga agngccncnt cgtataaccc ccctcncca       780
nccnacngnt agntcccccc cnggtnccg aangg                                  815
```

<210> 25
<211> 775
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(775)
<223> n = A,T,C or G

<400> 25

```
ccgagatgtc tcgctccgtg gccttagctg tgctcgcgct actctctctt tctggcctgg       60
aggctatcca gcgtactcca aagattcagg tttactcacg tcatccagca gagaatggaa      120
agtcaaattt cctgaattgc tatgtgtctg ggtttcatcc atccgacatt gaanttgact      180
tactgaagaa tgganagaga attgaaaaag tggagcattc agacttgtct ttcagcaagg      240
actggtcttt ctatctcntg tactacactg aattcacccc cactgaaaaa gatgagtatg      300
cctgccgtgt gaaccatgtg actttgtcac agcccaagat agttaagtgg gatcgagaca      360
tgtaagcagn cnncatggaa gtttgaagat gccgcatttg gattggatga attccaaatt      420
ctgcttgctt gcnttttaat antgatatgc ntatacaccc taccctttat gncccccaaat    480
tgtaggggtt acatnantgt tcncntngga catgatcttc ctttataant ccncentteg      540
aattgcccgt cnccengttn ngaatgtttc cnnaaccacg gttggctccc ccaggtcncc      600
tcttacggaa gggcctgggc cnctttncaa ggttggggga accnaaaatt tcncttntgc      660
ccnccccncca cnntcttgng nncncantt ggaaccctte cnattccccct tggcctcnna     720
ncttnncta anaaaacttn aaancgtngc naaannttn acttcccccc ttacc             775
```

<210> 26
<211> 820
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(820)
<223> n = A,T,C or G

<400> 26

```
anattantac agtgtaatct tttcccagag gtgtgtanag ggaacggggc ctagaggcat       60
cccanagata nettatanca acagtgcttt gaccaagagc tgctgggcac atttcctgca      120
gaaaaggtgg cggtccccat cactcctcct ctcccatagc catcccagag gggtgagtag      180
ccatcangcc ttcggtggga gggagtcang gaaacaacan acccacagagc anacagacca    240
ntgatgacca tgggcgggag cgagcctctt ccctgnaccg gggtggcana nganagccta      300
nctgaggggt cacactataa acgttaacga ccnagatnan cacctgcttc aagtgcaccc      360
ttcctacctg acnaccagng accnnnaact gcngcctggg gacagcnctg gganeagcta      420
acnnagcact cacctgcccc cccatggccg tccgcntccc tggtcctgnc aagggaagct      480
```

```
ccctgttgga attncgggga naccaaggga ncccccctcct ccanctgtga aggaaaaann      540
gatggaattt tnccctttccg gccnntcccc tcttcctttta cacgccccct nntactcatc      600
tccctctntt ntcctgncnc actttttnanc ccnnnatttc ccttnattga tcggaanncta     660
ganattccac tnacgcctnc cntcnatcng naanacnaaa nactntctna cccngggggat     720
gggnnectcg ntcatcctct cttttttcnct acnncnntt ctttgcctct ccttngatca       780
tccaacccntc gntggccntn ccccccnnn tcctttnccc                             820
```

<210> 27
<211> 818
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(818)
<223> n = A,T,C or G

<400> 27

```
tctgggtgat ggcctcttcc tcctcaggga cctctgactg ctctgggcca aagaatctct       60
tgtttcttct ccgagcccca ggcagcggtg attcagccct gccccaacctg attctgatga     120
ctgcggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggcgc      180
ctgctgagca cttccgcccc tcaccctgcc cagcccctgc catgagctct gggctgggtc      240
tccgcctcca gggttctgct cttccangca ngccancaag tggcgctggg ccacactggc      300
ttcttcctgc cccntccctg gctctgantc tctgtcttcc tgtcctgtgc angcncctg       360
gatctcagtt tccctcnctc anngaactct gtttctgann tcttcantta actntgantt      420
tatnaccnan tggnctgtnc tgtcnnactt taatgggccn gacggctaa tccctccctc       480
nctcccttcc anttcnnnna accngcttnc cntcntctcc ccntanccccg ccngggaanc     540
ctcctttgcc ctnaccangg gccnmnaccg cccatnncta gggggccnng gtnnctncnc      600
ctgntnnccc cncfcncnnt tncctcgtcc cnncnncgcn nngcannttc ncngtcccnn      660
tnnctcttcn ngtntcgnaa ngntcncntn tnnannqncn ngntnntncn tccctctcnc      720
cnnntgnang tnnttnnnnc ncagnncccc nnnncnnnnn nggnnntnnn tctncncngc      780
cccnncccc ngaattaagg cctccnntct ccggccnc                               818
```

<210> 28
<211> 731
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(731)
<223> n = A,T,C or G

<400> 28

```
aggaagggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg       60
tcccaacatg anggtgangt tctctttga angagggttg ngttttann ccnggtgggt        120
gattnaaccc cattgtatgg agnnaaaggn tttnagggat ttttcggctc ttatcagtat      180
ntanattcct gtnaatcgga aaatnatntt tcnncnggaa aatnttgctc ccatccgnaa      240
attnctcccg ggtagtgcat nttngggggn cngccangtt tcccaggctg ctanaatcgt      300
actaaagntt naagtgggan tncaaatgaa aacctancac agagnatccn tacccgactg      360
tnnnttncct tcgccctntg actctgcnng agcccaatac ccnngngnat gtcncccngn      420
nnngcgncnc tgaaannnnc tcgnggctnn gancatcang gggtttcgca tcaaaagcnn      480
cgtttcncat naaggcactt tngcctcatc caacencntag ccctcnncca tttngccgtc     540
ngcttcncct acgctnntng cncctnnntn ganattttac ccgcctnggg naancctcct      600
gnaatgggta gggncttntc ttttnaccnn gnggtntact aatcnnctnc acgcntnctt      660
tctcnacccc cccctttttt caatcccanc ggcnaatggg gtctcccnn cganggggg        720
nnnccanne c                                                            731
```

<210> 29
<211> 822
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(822)
<223> n = A,T,C or G

<400> 29
actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat 60
cgctcanacc tcacancctc ccnacnangc ctataangaa nannaataga cctgtncnnt 120
atatntacnc tcatannoct cnnnacccac tccctcttaa cccntactgt gcctatngcn 180
tnnctantct ntgccgcctn cnanccaccn gtgggccnac cncnngnatt ctcnatctcc 240
tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300
tccatnantt annntaacta ccactgacnt ngactttcnc atnanctcct aatttgaatc 360
tactctgact cccacngcct annnattagc ancntccccc nacnatntct caaccaaatc 420
ntcaacaacc tatctanctg ttcnccaacc nttncctccg atccccnnac aaccccccto 480
ccaaataccc nccacctgac ncctaacccn caccatcccg gcaagccnan ggncatttan 540
ccactggaat cacnatngga naaaaaaaac ccnaactctc tancncnnat ctccctaana 600
aatnctcctn aaatttactn ncantnccat caancccacn tgaaacnnaa ccccctgtttt 660
tanatccctt ctttcgaaaa ccnaccottt annnccccac ctttnggggcc ccccncnctnc 720
ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaggcna ananonntccg 780
canatcctat cccttanttn ggggnccctt nccengggcc cc 822

<210> 30
<211> 787
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(787)
<223> n = A,T,C or G

<400> 30
cggccgcctg ctctggcaca tgcctcctga atggcatcaa aagtgatgga ctgcccattg 60
ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120
gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna 180
gctggaagcc ctggagggcc tctctcgcca gcctccccct tctctccacg ctctccangg 240
acaccagggg ctccaggcag cccattattc ccagnangac atggtgtttc tccacgcgga 300
cccatggggc ctgnaaggcc agggtctcct ttgacaccat ctctcccgtc ctgcctggca 360
ggccgtggga tccactantt ctanaacggn cgccaccncg gtgggagctc cagcttttgt 420
tcccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt 480
gtgaaattgt ttntccccctc ncnattccnc ncnacatacn aacccggaan cataaagtgt 540
taaagcctgg gggtngcctn nngaatnaac tnaactcaat taattgcgtt ggctcatggc 600
ccgctttccn ttcnggaaaa ctgtcntccc ctgcnttnnt gaatcggcca cccccngggg 660
aaaagcggtt tgcnttttng ggggntcctt ccncttcccc cctcnctaan ccctncgcct 720
cggtcgttnc nggtngcggg gaangggnat nnnctcccnc naaggggggng agnnngntat 780
ccccaaa 787

<210> 31
<211> 799
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(799)
<223> n = A,T,C or G

<400> 31
tttttttttt ttttttttggc gatgctactg tttaattgca ggaggtgggg gtgtgtgtac 60
catgtaccag ggctattaga agcaagaagg aaggagggag ggcagagcgc cctgctgagc 120
aacaaaggac tcctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct 180
cccgcagggt gggggccacc agtccagggg tgggagcact acanggggtg ggagtgggtg 240
gtggctggtn cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca 300
ggggaccttc tgttctccca nggnaacttc ntnnatctcn aaagaacaca actgtttctt 360
cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttggtaca 420
tatggttccg gcccacctct cccntcnaan aagtaattca cccccccccn ccntctnttg 480
cctgggccct taantaccca cacccggaact canttantta ttcatcttng gntgggcttg 540
ntnatcnacn cctgaangcg ccaagttgaa aggccacgcc gtnacccnctc cccatagnan 600
nttttnncnt canctaatgc cccccngggc aacnatccaa tcccccccn tgggggcccc 660
agccccanggc ccccgnctcg ggnnnccngn cncgnantcc ccaggntctc ccantcngnc 720
ccnnngcncc cccgcacgca gaacanaagg ntngagccnc cgcannnnnn nggtnncnac 780
ctcgcccccc ccnnncgnng 799

<210> 32
<211> 789
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(789)
<223> n = A,T,C or G

<400> 32
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
ttttnccnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac 120
ggcaacaggc tccggcggcg gcggcggcgg ccctacctgc ggtaccaaat ntgcagcctc 180
cgctcccgct tgatattcct ctgcagctgc aggatgccnt aaaacagggc ctcggccntn 240
ggtgggcacc ctgggatttn aatttnccacg ggcacaatgc ggtcgcancc cctcaccacc 300
nattaggaat agtggtntta cccncccnccg ttggcncact ccccntggaa accacttntc 360
gcggctccgg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt 420
nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancn ccccaaaacc 480
ggnccatgtc ttnncggggt tgctgcnatn tncatcacct cccgggcnca ncaggncaac 540
ccaaaagttc ttgnggcccn caaaaaanct ccgggggggnc ccagtttcaa caaagtcatc 600
cccttggcc cccaaatcct ccccccgntt nctgggtttg ggaacccacg cctctnnctt 660
tggnnggcaa gntggntccc ccttcgggcc cccggtgggc ccnnctctaa ngaaaacncc 720
ntcctnnnca ccatcccccc nngnnacgnc tancaangna tccctttttt tanaaacggg 780
cccccncg 789

<210> 33
<211> 793
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(793)
<223> n = A,T,C or G

<400> 33
gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg 60

aattcatggc tgttggagca atanaacccc agttctacga gctgctgatc aaaggacttg 120
gactaaagtc tgatgaactt cccaatcaga tgagcatgga tgattggcca gaaatgaana 180
agaagtttgc agatgtattt gcaaagaaga cgaaggcaga gtggtgtcaa atctttgacg 240
gcacagatgc ctgtgtgact ccggttctga cttttgagga ggttgttcat catgatcaca 300
acaangaacg gggctcgttt atcaccantg aggagcagga cgtgagcccc cgccctgcac 360
ctctgctgtt aaacacccca gccatccctt ctttcaaaag ggatccacta cttctagagc 420
ggncgccacc gcggtggagc tccagctttt gttcccttta gtgagggtta attgcgcgct 480
tggcgtaatc atggtcatan ctgtttcctg tgtgaaattg ttatccgctc acaattccac 540
acaacatacg anccggaagc atnaaatttt aaagcctggn ggtngcctaa tgantgaact 600
nactcacatt aattggcttt gcgctcactg cccgctttcc agtccggaaa acctgtcctt 660
gccagctgcc nttaatgaat cnggccaccc cccgggaaa aggcngtttg cttnttgggg 720
cgcncttccc gctttctcgc ttcctgaant ccttcccccc ggtctttcgg cttgcggcna 780
acggtatcna cct 793

<210> 34
<211> 756
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(756)
<223> n = A,T,C or G

<400> 34
gccgcgaccg gcatgtacga gcaactcaag ggcgagtgga accgtaaaag ccccaatctt 60
ancaagtgcg gggaanagct gggtcgactc aagctagttc ttctggagct caacttcttg 120
ccaaccacag ggaccaagct gaccaaacag cagctaattc tggcccgtga catactggag 180
atcgggggcc aatggagcat cctacgcaan gacatcccct ccttcgagcg ctacatggcc 240
cagctcaaat gctactactt tgattacaan gagcagctcc ccgagtcagc ctatatgcac 300
cagctcttgg gcctcaacct cctcttcctg ctgtcccaga accgggtggc tgantnccac 360
acggantttg ancggctgcc tgcccaanga catacanacc aatgtctaca tcnaccacca 420
gtgtcctgga gcaatactga tgganggcag ctacccncaaa gtnttcctgg ccnagggtaa 480
catccccgc cgagagctac acctcttca ttgacatcct gctcgacact atcagggatg 540
aaaatcgcng ggttgctcca gaaaggctnc aanaanatcc ttttcnctga aggcccccgg 600
atncnctagt nctagaatcg gcccgccatc gcggtgganc ctccaacctt tcgttnccct 660
ttactgaggg ttnattgccg cccttggcgt tatcatggtc acnccagttn cctgtgttga 720
aattnttaac ccccacaat tccacgccna cattng 756

<210> 35
<211> 834
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(834)
<223> n = A,T,C or G

<400> 35
ggggatctct anatcnacct gnatgcatgg ttgtcggtgt ggtcgctgtc gatgaanatg 60
aacaggatct tgcccttgaa gctctcggct gctgtntttta agttgctcag tctgccgtca 120
tagtcagaca cnctcttggg camaaaacan caggatntga gtcttgattt cacctccaat 180
aatcttcngg gctgtctgct cggtgaactc gatgacnang ggcagctggt tgtgtntgat 240
aaantccanc angttctcct tggtgacctc cccttcaaag ttgttccggc cttcatcaaa 300
cttctnnaan angannancc canctttgtc gagctggnat ttgganaaca cgtcactgtt 360
ggaaactgat cccaaatggt atgtcatcca tcgcctctgc tgcctgcaaa aaacttgctt 420
ggcncaaatc cgactcccn tccttgaaag aagccnatca cacccccctc cctggactcc 480

```
nncaangact ctaccgctnc cccntccnng cagggttggt ggcannccgg gcccntgcgc      540
ttcttcagcc agttcacnat gttcatcagc ccctctgcca gcrgttntat tccttggggg      600
ggaanccgtc tctcccttcc tgaannaact ttgaccgtag gaatagccgc gcntcncccnt     660
acntnctggg ccgggttcaa antccctccn ttgncantcn cctcgggcca ttctggattt      720
nccnaacttt ttccttcccc cnccccncgg ngtttggntt tttcatnggg ccccaactct      780
gctnttggcc antcccctgg gggcntntan cncccccntnt ggtcccntag ggcc           834
```

<210> 36
<211> 814
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(814)
<223> n = A,T,C or G

<400> 36

```
cggncgcttt ccngccgcgc cccgtttcca tgacnaaggc tcccttcang ttaaatacnn       60
cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgccca      120
naacgccaac tcaggccatt cctaccaaag gaagaaaggc tggtctctcc acccctgta       180
ggaaaggcct gccttgtaag acaccacaat ncggctgaat ctnaagtctt gtgttttact      240
aatggaaaaa aaaaataaac aanaggtttt gttctcatgg ctgcccaccg cagcctggca      300
ctaaaacanc ccagcgctca cttctgcttg ganaaatatt ctttgctctt ttggacatca      360
ggcttgatgg tatcactgcc acntttccac ccagctgggc nccctttcccc catntttgtc     420
antganctgg aaggcctgaa nettagtctc caaaagtctc ngcccacaag acrggccacc      480
aggggangtc ntttncagtg gatctgccaa ananntaccn tatcatcant gaataaaaag      540
gcccctgaac ganatgcttc cancanccttt taagacccat aatcctngaa ccatggtgcc     600
cttccggtct gatccnaaag gaatgttcct gggtcccant ccctcctttg ttncttacgt      660
tgtnttggac cntgctngn atnacccaan tganatcccc agaagcaccc tnccccctggc      720
atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcnccnaan      780
ggngaactca agaaggtctn ngaaaaacca cncn                                  814
```

<210> 37
<211> 760
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(760)
<223> n = A,T,C or G

<400> 37

```
gcatgctgcc cttcctcaaa gttgttcttg ttgccatcac aaccaccata ggtaaagcgg       60
gcgcagtgtt cgctgaaggg gttgtagtac cagcgcggga tgctctcctt gcagagtcct      120
gtgtctggca ggtccacgca atgccctttg tcactgggga aatggatgcg ctggagctcg      180
tcnaanccac tcgtgtattt ttcacangca gcctcctccg aagcntccgg gcagttgggg      240
gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt      300
gggctgacag gtgccagaac acactggatn ggcctttcca tggaagggcc tgggggaaat      360
cncctnancc caaactgcct ctcaaaggcc accttgcaca ccccgacagg ctagaaatgc      420
actcttcttc ccaaaggtag ttgttcttgt tgccaagca ncctccanca aaccaaanc        480
ttgcaaaatc tgctccgtgg gggtcatnnn taccanggtt ggggaaanaa acncggcngn      540
ganccncctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaanagca      600
caattgaact gttaacnttg ggccgngttc cnctnggggtg gtctgaaact aatcaccgtc     660
actggaaaaa ggtangtgcc ttccttgaat tccccaaantt cccctngntt tgggtnntt      720
ctcctctncc ctaaaaatcg tnttcccccc ccntanggcg                            760
```

<210> 38
<211> 724
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(724)
<223> n = A,T,C or G

<400> 38
tttttttttt tttttttttt tttttttttt tttttaaaaa ccccctccat tgaatgaaaa 60
cttccaaaat tgtccaaccc cctcnnccaa atnnccattt ccgggggggg gttccaaacc 120
caaattaatt ttgganttta aattaaatnt tnattngggg aanaanccaa atgtnaagaa 180
aatttaaccc attatnaact taaatnccta gaaacccntg gnttccaaaa attttaacc 240
cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaaggtt 300
ngatttaaac cccttnant tnttttnacc cnagnctnaa ntattngnt tccggtgttt 360
tcctnttaan cntnggtaac tcccgntaat gaannncccct aanccaatta aaccgaattt 420
ttttgaatt ggaattccn ngggaattna ccggggtttt tcccnttgg gggccatncc 480
cccnctttcg gggtttgggn ntaggttgaa tttttnnang ncccaaaaaa nccccccaana 540
aaaaaactcc caagnnttaa ttngaatntc cccttccca ggccttttgg gaaaggnggg 600
tttntggggg ccngggantt cnttcccccn ttnccncccc cccccnggt aaanggttat 660
ngnntttggt ttttgggccc cttnanggac cttccggatn gaaattaaat ccccgggncg 720
gccg 724

<210> 39
<211> 751
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(751)
<223> n = A,T,C or G

<400> 39
tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca 60
caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt 120
tttatttatt tttactgaaa gtgagaggga actttttgtgg cctttttttcc tttttctgta 180
ggccgcctta agctttctaa atttggaaca tctaagcaag ctgaanggaa aaggggttt 240
cgcaaaatca ctcgggggaa aggaaaggtt gctttgttaa tcatgcccta tggtgggtga 300
ttaactgctt gtacaattac atttcacttt taattaattg tgctnaangc tttaattana 360
cttggggggtt ccctccccan accaaccccn ctgacaaaaa gtgccngccc tcaaatnatg 420
tcccggcnnt cnttgaaaca cacngcngaa ngttctcatt atcccncnc caggtnaaaa 480
tgaagggtta ccatntttaa cnccacctcc acntggcnnn gcctgaatcc tcnaaaancn 540
ccctcaancn aattnctnng ccccggtcnc gcntnngtcc cnccccgggct ccgggaantn 600
caccccnga anncanntnnc nnacnaaatt ccgaaatat tcccnntcnc tcaattcccc 660
cnnagactnt cctcnnncnan cncaattttc ttttnntcac gaacncgnnc cnnaaaatgn 720
nnnncncctc cnctngtccn naatcnccan c 751

<210> 40
<211> 753
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(753)